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RAW SEQUENCE LISTING

DATE: 03/11/2002

PATENT APPLICATION: US/09/785,689A

TIME: 09:49:53

Input Set : A:\EP.txt

Output Set: N:\CRF3\03112002\I785689A.raw

SEQUENCE LISTING

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4 (1) GENERAL INFORMATION:
6   (i) APPLICANT: Lindler, Luther E
7           Warren, Richard
8           VanDeBerg, Lillian
9           Rubin, Fran
11  (ii) TITLE OF INVENTION: Protein From Brucella Species
13  (iii) NUMBER OF SEQUENCES: 2
15  (iv) CORRESPONDENCE ADDRESS:
16        (A) ADDRESSEE: Hendricks and Associates
17        (B) STREET: P.O. Box 2509
18        (C) CITY: Fairfax
19        (D) STATE: Virginia
20        (E) COUNTRY: United States
21        (F) ZIP: 22031
23  (v) COMPUTER READABLE FORM:
24        (A) MEDIUM TYPE: Floppy disk
25        (B) COMPUTER: IBM PC compatible
26        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
29  (vi) CURRENT APPLICATION DATA:
C--> 30        (A) APPLICATION NUMBER: US/09/785,689A
C--> 31        (B) FILING DATE: 20-Feb-2001
32        (C) CLASSIFICATION:
34  (viii) ATTORNEY/AGENT INFORMATION:
35        (A) NAME: Hendricks, Glenna
36        (B) REGISTRATION NUMBER: 32,535
37        (C) REFERENCE/DOCKET NUMBER: lindler
39  (ix) TELECOMMUNICATION INFORMATION:
40        (A) TELEPHONE: (703) 425-8405
41        (B) TELEFAX: (703) 425-8406
44 (2) INFORMATION FOR SEQ ID NO: 1:
46   (i) SEQUENCE CHARACTERISTICS:
47        (A) LENGTH: 1025 base pairs
48        (B) TYPE: nucleic acid
49        (C) STRANDEDNESS: single
50        (D) TOPOLOGY: unknown
52   (ii) MOLECULE TYPE: DNA (genomic)
54   (iii) HYPOTHETICAL: NO
56   (iv) ANTI-SENSE: NO
58   (vi) ORIGINAL SOURCE:
59        (A) ORGANISM: Brucella
62   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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64 CCCCTGACAT AACCCGCTTT GTCCAAATTT TTTCAACTTT TCCTGTAGGA GATTTTATGA      60
66 ACACTCGTGC TAGCAATTTT CTCGCAGCCT CATTTTCCAC AATCATGCTC GTCGGCGCTT      120
68 TCAGCCTGCC CGCTTTCGCA CAGGAGAATC AGATGACGAC GCAGCCCGCG CGCATCGCCG      180
70 TCACCGGGGA AGGCATGATG ACGGCCCTCGC CCGATATGGC CATTCTCAAT CTCTCGGTGC      240
72 TACGCCAGGC AAAGACCGCG CGCGAAGCCA TGACCGCGAA TAATGAAGCC ATGACAAAAG      300
74 TGCTCGATGC CATGAAGAAG GCCGGCATCG AAGATCGCGA TCTCCAGACA GCGGGCATCA      360
76 ATATCCAGCC GATTTATGTC TATCCTGACG ACAAGAACAA CCTGAAAGAG CCTACCATCA      420
78 CCGGCTATTC TGTATCCACC AGTCTCACGG TTCGCGTGCG CGAACTGGCC AATGTTGGAA      480
80 AAATTTTGGA TGAATCCGTC ACGCTCGGTG TTAATCAGGG CGGTGATTTG AACCTGGTCA      540
82 ATGATAATCC CTCCGCCGTG ATCAACGAGG CGCGCAAGCG CGCAGTGGCC AATGCCATTG      600
84 CCAAGGCGAA GACGCTTGCC GACGCTGCAG GCGTGGGGCT TGGCCGTGTG GTGGAAATCA      660
86 GTGAAGTGAAG CCGCCCGCCC ATGCCGATGC CAATTGCGCG CGGACAGTTC AGAACCATGC      720
88 TAGCAGCCGC ACCGGACAAT TCCGTGCCGA TTGCCGAGG CGAAAACAGC TATAACGTAT      780
90 CGGTCAATGT CGTTTTTGAA ATCAAGTAAA TAGCTGGGGT ATGACGCCCT TTGCCACCTG      840
92 ATACAAAACG CCGGCCTGGT TTCACAGGCC GGTTTTTTTG ATTAGAGCGC GTTTCGATCT      900
94 GATTGAATCC GATCGGCGCT CTAATCCTTT GTTTGTACGC GCATCTTTTC CGAAAACCGT      960
96 TTCACACTTT TCGGGATGCG GTCTAGCGGA TGATCGGGCA ACCGCGCGTA TCGGCAAATG      1020
98 TCACG      1025

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100 (2) INFORMATION FOR SEQ ID NO: 2:

102 (i) SEQUENCE CHARACTERISTICS:

103 (A) LENGTH: 250 amino acids

104 (B) TYPE: amino acid

105 (C) STRANDEDNESS: single

106 (D) TOPOLOGY: unknown

108 (ii) MOLECULE TYPE: protein

110 (iii) HYPOTHETICAL: NO

112 (iv) ANTI-SENSE: NO

114 (v) FRAGMENT TYPE: internal

116 (vi) ORIGINAL SOURCE:

117 (A) ORGANISM: Brucella

118 (B) STRAIN: unknown

121 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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123 Met Asn Thr Arg Ala Ser Asn Phe Leu Ala Ser Phe Ser Thr Ile
124 1 5 10 15
126 Met Leu Val Gly Ala Phe Ser Leu Pro Ala Phe Ala Gln Glu Asn Gln
127 20 25 30
129 Met Thr Thr Gln Pro Ala Arg Ile Ala Val Thr Gly Glu Gly Met Met
130 35 40 45
132 Thr Ala Ser Pro Asp Met Ala Ile Leu Asn Leu Ser Val Leu Arg Gln
133 50 55 60
135 Ala Lys Thr Ala Arg Glu Ala Met Thr Ala Asn Asn Glu Ala Met Thr
136 65 70 75 80
138 Lys Val Leu Asp Ala Met Lys Lys Ala Gly Ile Glu Asp Arg Asp Leu
139 85 90 95
141 Gln Thr Gly Gly Ile Asn Ile Gln Pro Ile Tyr Val Tyr Pro Asp Asp
142 100 105 110
144 Lys Asn Asn Leu Lys Glu Pro Thr Ile Thr Gly Tyr Ser Val Ser Thr
145 115 120 125
147 Ser Leu Thr Val Arg Val Arg Glu Leu Ala Asn Val Gly Lys Ile Leu

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148		130		135		140													
150	Asp	Glu	Ser	Val	Thr	Leu	Gly	Val	Asn	Gln	Gly	Gly	Asp	Leu	Asn	Leu			
151	145					150					155					160			
153	Val	Asn	Asp	Asn	Pro	Ser	Ala	Val	Ile	Asn	Glu	Ala	Arg	Lys	Arg	Ala			
154				165						170					175				
156	Val	Ala	Asn	Ala	Ile	Ala	Lys	Ala	Lys	Thr	Leu	Ala	Asp	Ala	Ala	Gly			
157			180						185					190					
159	Val	Gly	Leu	Gly	Arg	Val	Val	Glu	Ile	Ser	Glu	Leu	Ser	Arg	Pro	Pro			
160		195						200					205						
162	Met	Pro	Met	Pro	Ile	Ala	Arg	Gly	Gln	Phe	Arg	Thr	Met	Leu	Ala	Ala			
163		210					215					220							
165	Ala	Pro	Asp	Asn	Ser	Val	Pro	Ile	Ala	Ala	Gly	Glu	Asn	Ser	Tyr	Asn			
166	225					230					235					240			
168	Val	Ser	Val	Asn	Val	Val	Phe	Glu	Ile	Lys									
169				245						250									

VERIFICATION SUMMARY

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]